Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 08:32:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716716.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR9716716 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716716.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 08:32:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716716.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,789,173
Mapped reads	1,512,380 / 84.53%
Unmapped reads	276,793 / 15.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,337 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	40,797 / 2.28%
Duplication rate	2.05%
Clipped reads	1,514,952 / 84.67%

2.2. ACGT Content

Number/percentage of A's	21,591,801 / 25.24%
Number/percentage of C's	15,094,298 / 17.65%
Number/percentage of T's	26,863,106 / 31.41%
Number/percentage of G's	21,986,433 / 25.7%
Number/percentage of N's	1,768 / 0%
GC Percentage	43.35%

2.3. Coverage

Mean	0.0276

Standard Deviation	0.2216

2.4. Mapping Quality

Mean Mapping Quality	43.94

2.5. Mismatches and indels

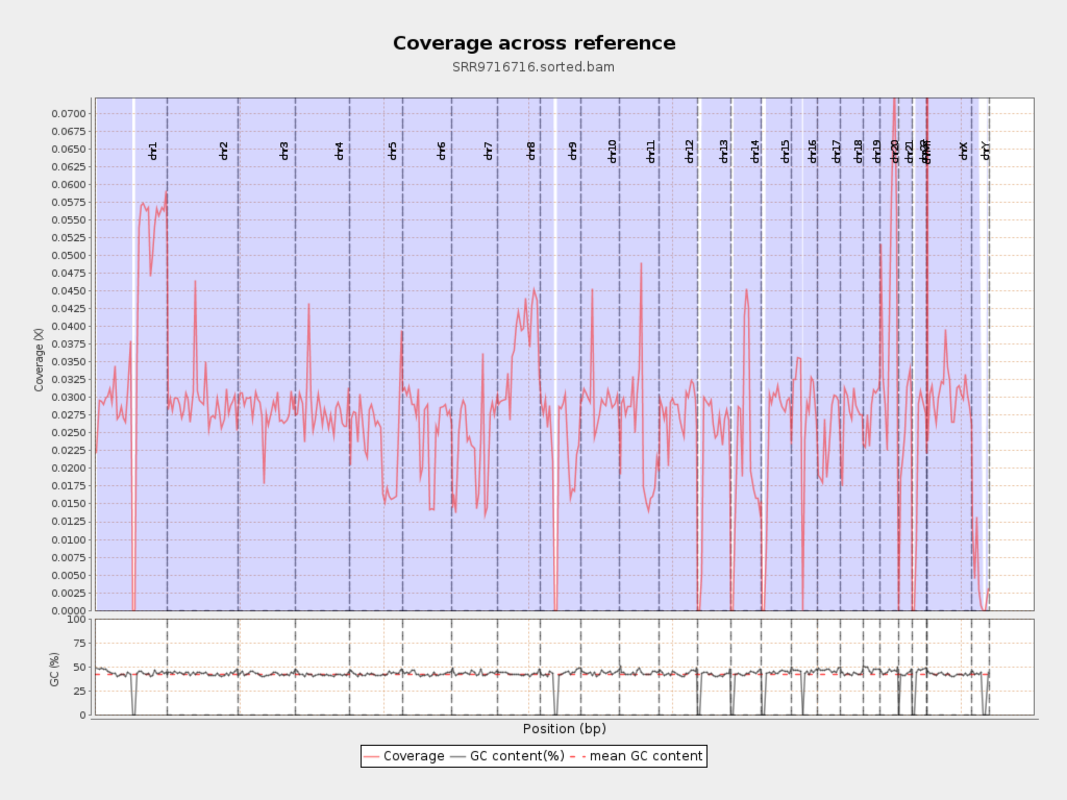
General error rate	0.5%
Mismatches	421,259
Insertions	5,416
Mapped reads with at least one insertion	0.36%
Deletions	13,345
Mapped reads with at least one deletion	0.88%
Homopolymer indels	40.83%

2.6. Chromosome stats

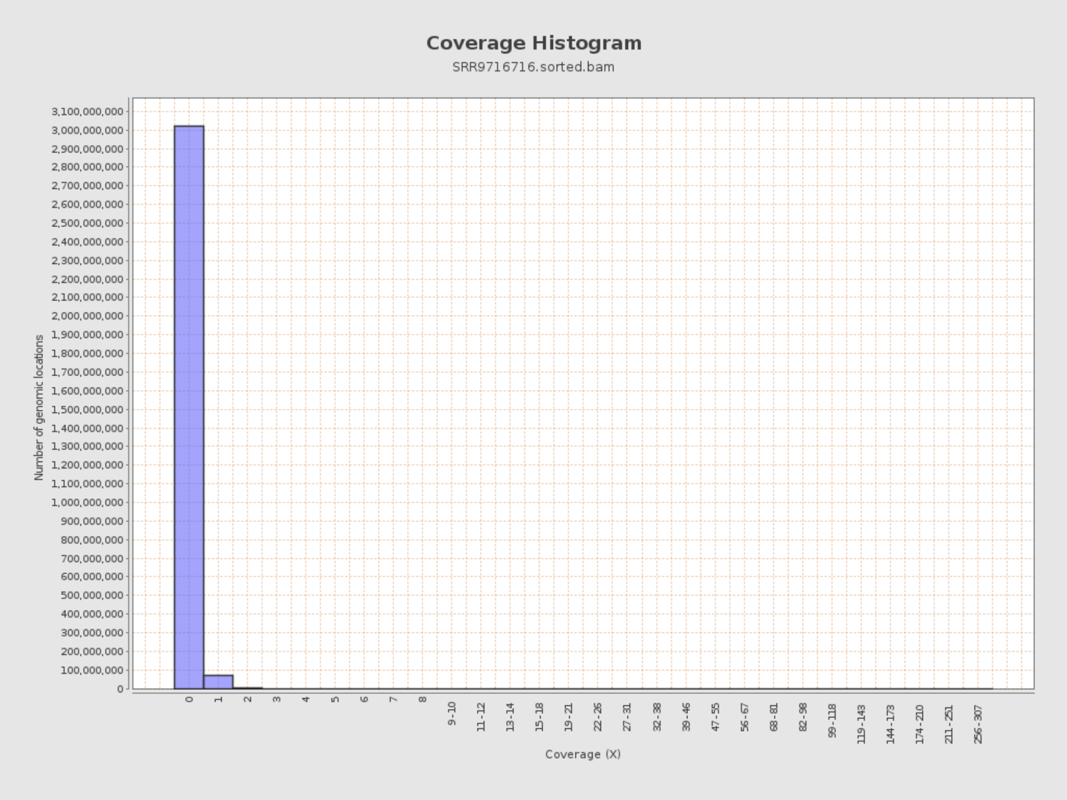
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9541264	0.0383	0.3087
chr2	243199373	7150890	0.0294	0.2504
chr3	198022430	5588194	0.0282	0.1827
chr4	191154276	5425755	0.0284	0.1976
chr5	180915260	4319949	0.0239	0.1694
chr6	171115067	4438069	0.0259	0.1862
chr7	159138663	3694648	0.0232	0.2027

chr8	146364022	5382374	0.0368	0.2311
chr9	141213431	3116000	0.0221	0.2298
chr10	135534747	4045961	0.0299	0.243
chr11	135006516	3413881	0.0253	0.2215
chr12	133851895	3798482	0.0284	0.1866
chr13	115169878	2602148	0.0226	0.162
chr14	107349540	2336073	0.0218	0.1742
chr15	102531392	2454158	0.0239	0.1687
chr16	90354753	2515997	0.0278	0.1969
chr17	81195210	1970560	0.0243	0.1759
chr18	78077248	2136476	0.0274	0.4205
chr19	59128983	1651713	0.0279	0.2367
chr20	63025520	2782446	0.0441	0.2376
chr21	48129895	1161384	0.0241	0.1846
chr22	51304566	1029058	0.0201	0.1537
chrMT	16571	18907	1.141	1.277
chrX	155270560	4738970	0.0305	0.2153
chrY	59373566	246506	0.0042	0.1016

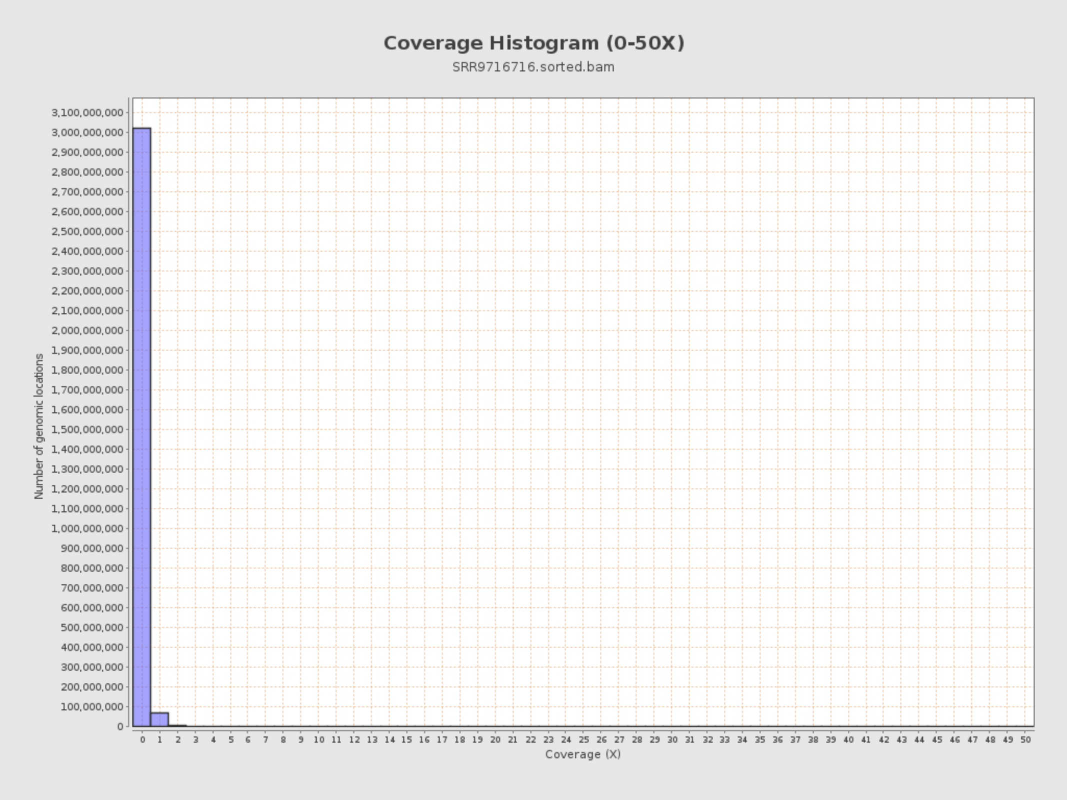
3. Results : Coverage across reference



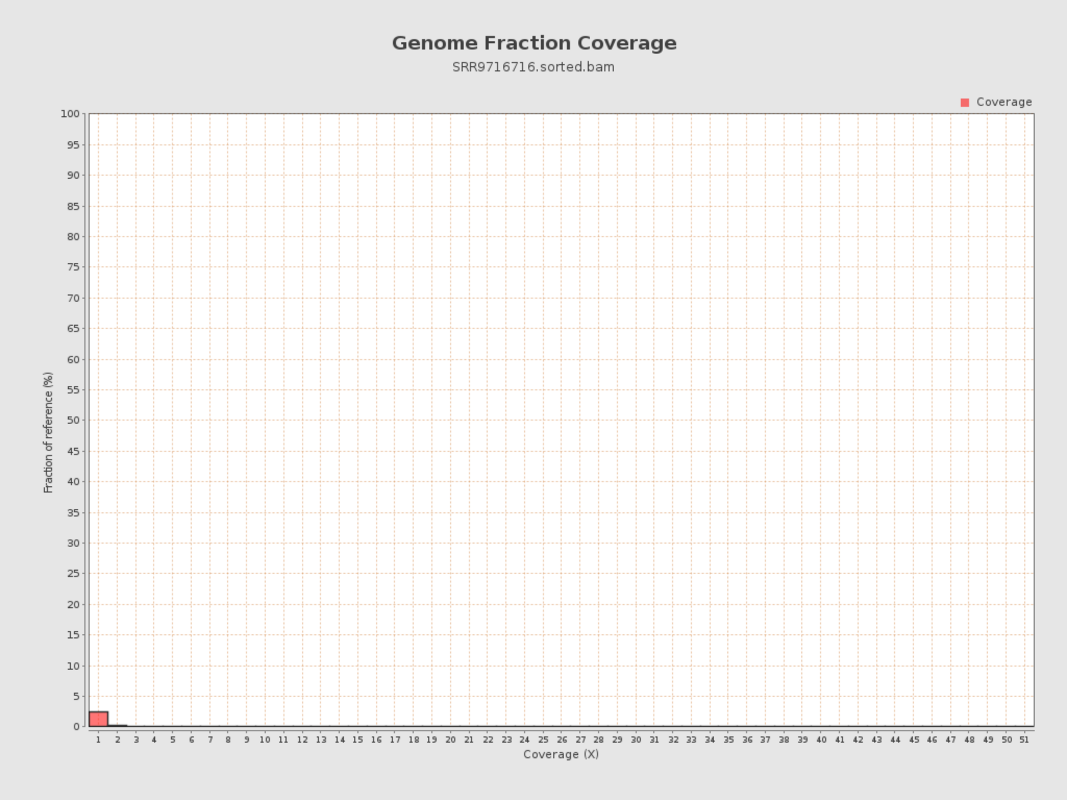
4. Results : Coverage Histogram



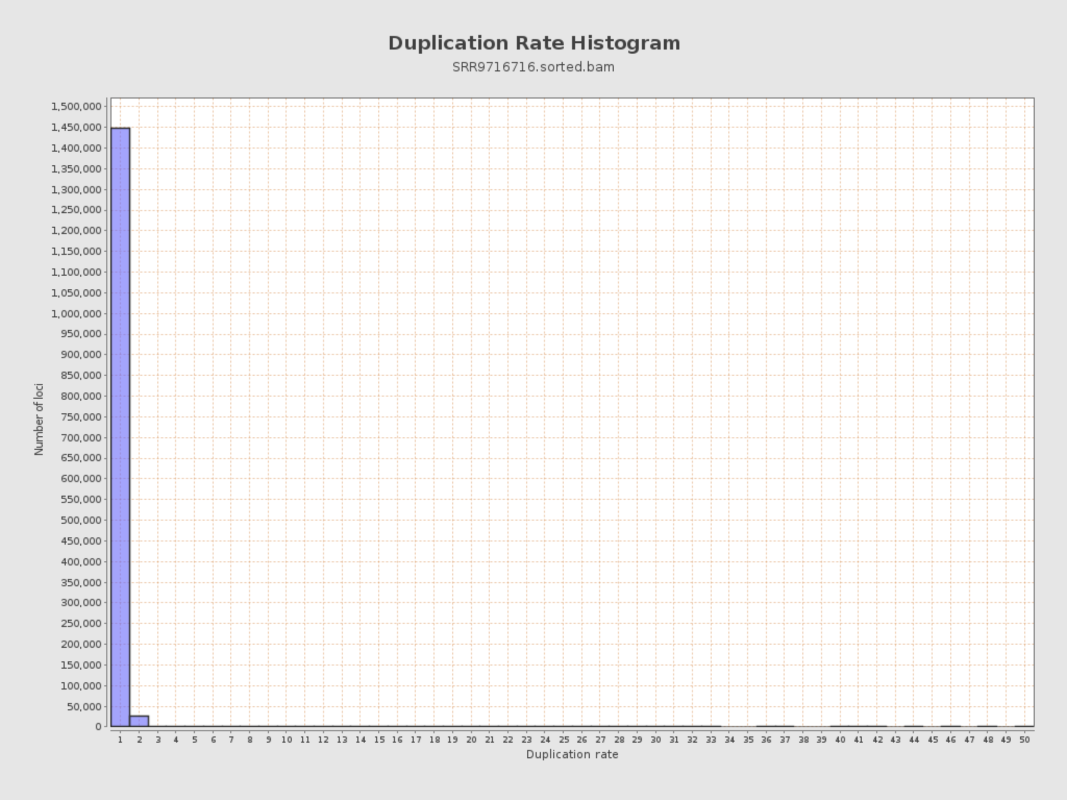
5. Results : Coverage Histogram (0-50X)



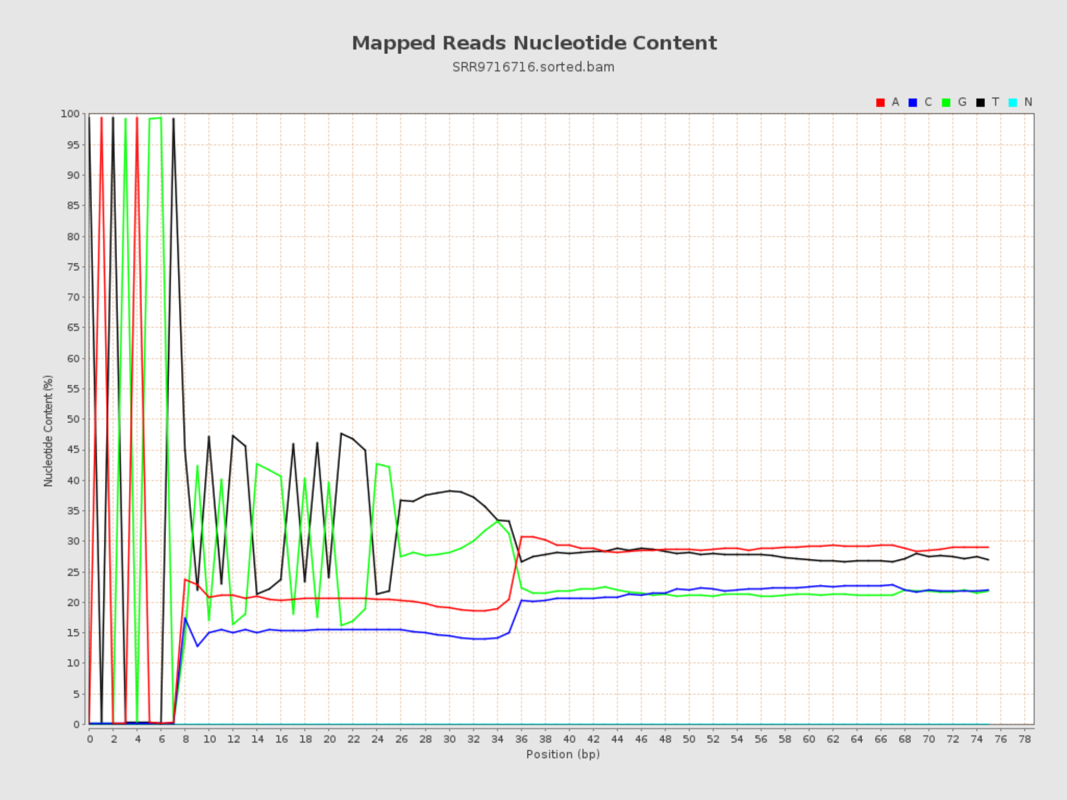
6. Results : Genome Fraction Coverage



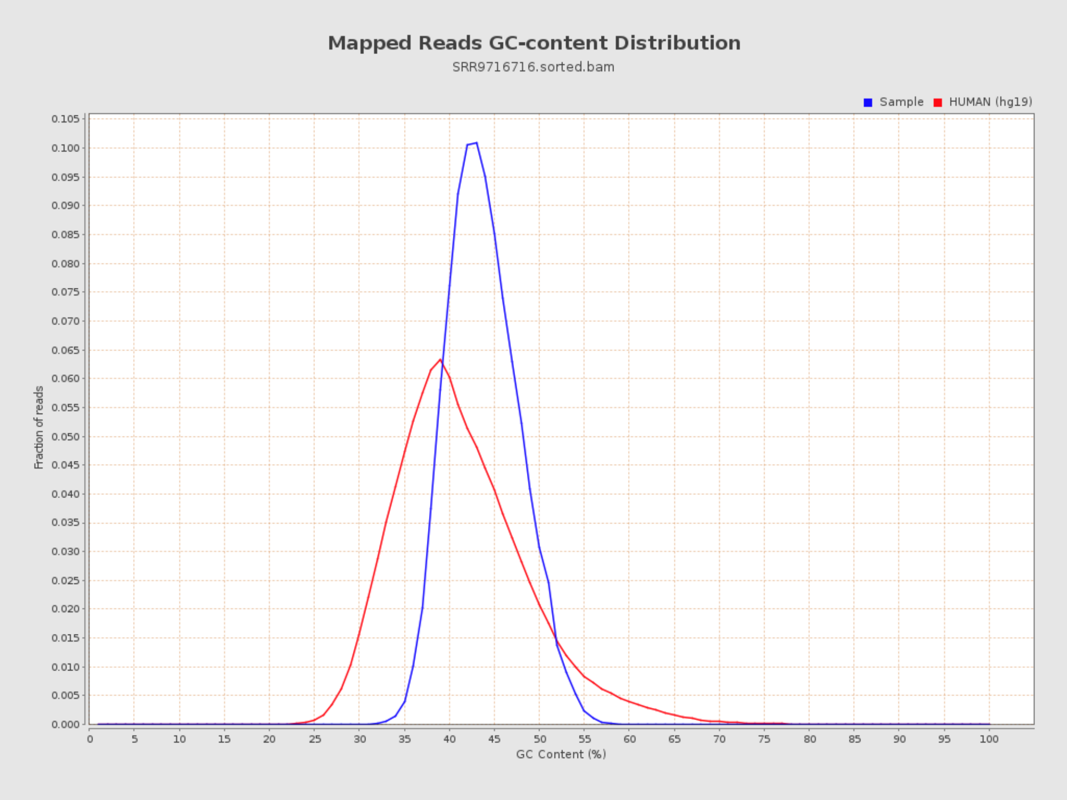
7. Results : Duplication Rate Histogram



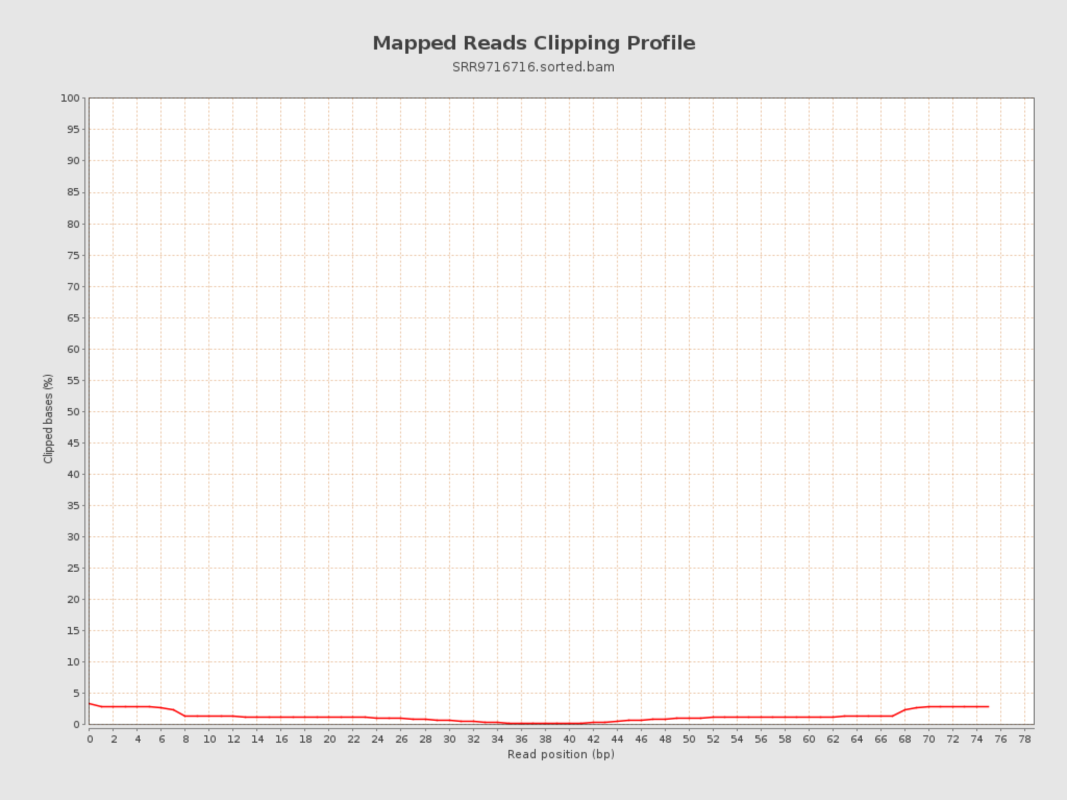
8. Results : Mapped Reads Nucleotide Content



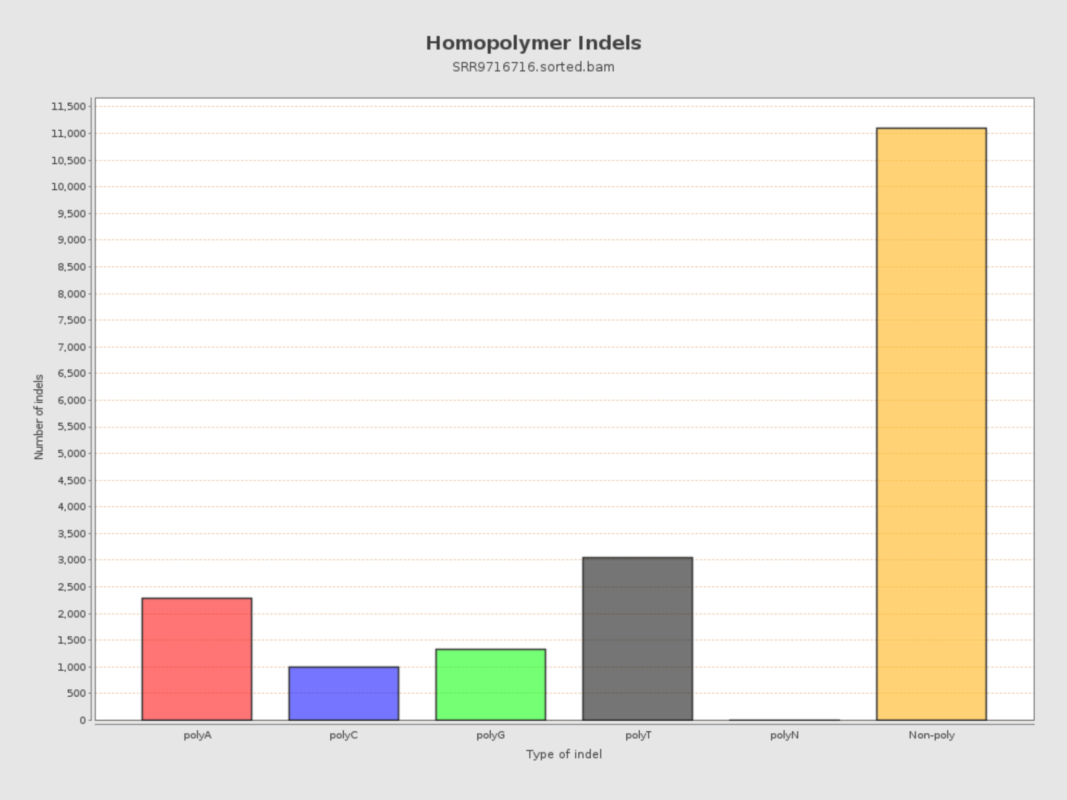
9. Results : Mapped Reads GC-content Distribution



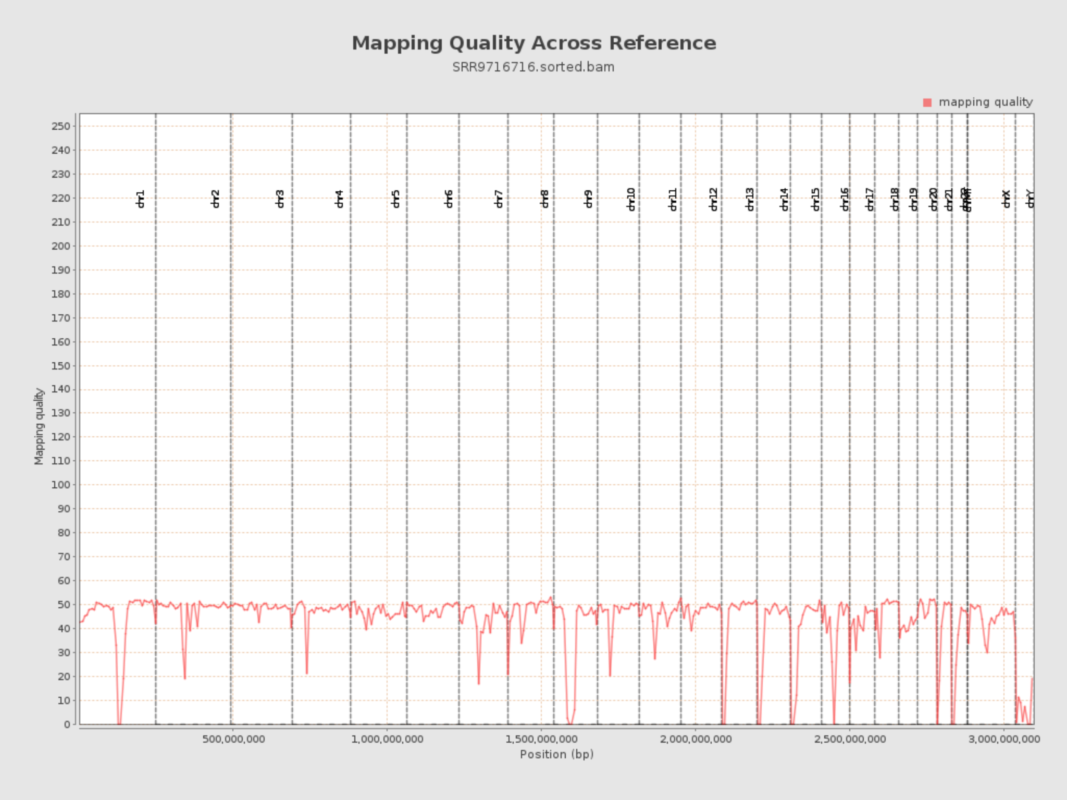
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram